

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/936,190

DATE: 10/04/2001

TIME: 15:29:01

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Output Set: N:\CRF3\10042001\I936190.raw

3 <110> APPLICANT: STEELE, Christopher L.
 4 DIXON, Richard A.
 6 <120> TITLE OF INVENTION: GENETIC MANIPULATION OF ISOFLAVONOID
 8 <130> FILE REFERENCE: 11137/05006
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/936,190
 C--> 11 <141> CURRENT FILING DATE: 2001-09-13
 13 <150> PRIOR APPLICATION NUMBER: 60/123,267
 14 <151> PRIOR FILING DATE: 1999-03-08
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1717
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Glycine max
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (36)..(1598)
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 32 1 5
 34 ctt ggt tta ttg gtt ttg gct ctg ttt ctg cac ttg cgt ccc aca ccc 101
 35 Leu Gly Leu Leu Val Leu Ala Leu Phe Leu His Leu Arg Pro Thr Pro
 36 10 15 20
 38 act gca aaa tca aaa gca ctt cgc cat ctc cca aac cca cca agc cca 149
 39 Thr Ala Lys Ser Lys Ala Leu Arg His Leu Pro Asn Pro Pro Ser Pro
 40 25 30 35
 42 aag cct cgt ctt ccc ttc ata gga cac ctt cat ctc tta aaa gac aaa 197
 43 Lys Pro Arg Leu Pro Phe Ile Gly His Leu His Leu Leu Lys Asp Lys
 44 40 45 50
 46 ctt ctc cac tac gca ctc atc gac ctc tcc aaa aaa cat ggt ccc tta 245
 47 Leu Leu His Tyr Ala Leu Ile Asp Leu Ser Lys Lys His Gly Pro Leu
 48 55 60 65 70
 50 ttc tct ctc tac ttt ggc tcc atg cca acc gtt gtt gcc tcc aca cca 293
 51 Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro
 52 75 80 85
 54 gaa ttg ttc aag ctc ttc ctc caa acg cac gag gca act tcc ttc aac 341
 55 Glu Leu Phe Lys Leu Phe Leu Gln Thr His Glu Ala Thr Ser Phe Asn
 56 90 95 100
 58 aca agg ttc caa acc tca gcc ata aga cgc ctc acc tat gat agc tca 389
 59 Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg Leu Thr Tyr Asp Ser Ser
 60 105 110 115
 62 gtg gcc atg gtt ccc ttc gga cct tac tgg aag ttc gtg agg aag ctc 437
 63 Val Ala Met Val Pro Phe Gly Pro Tyr Trp Lys Phe Val Arg Lys Leu
 64 120 125 130
 66 atc atg aac gac ctt ctc aac gcc acc act gta aac aag ttg agg cct 485
 67 Ile Met Asn Asp Leu Leu Asn Ala Thr Thr Val Asn Lys Leu Arg Pro

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71	Leu	Arg	Thr	Gln	Gln	Ile	Arg	Lys	Phe	Leu	Arg	Val	Met	Ala	Gln	Gly	
72					155					160					165		
74	gca	gag	gca	cag	aag	ccc	ctt	gac	ttg	acc	gag	gag	ctt	ctg	aaa	tgg	581
75	Ala	Glu	Ala	Gln	Lys	Pro	Leu	Asp	Leu	Thr	Glu	Glu	Leu	Leu	Lys	Trp	
76				170				175						180			
78	acc	aac	agc	acc	atc	tcc	atg	atg	atg	ctc	ggc	gag	gct	gag	gag	atc	629
79	Thr	Asn	Ser	Thr	Ile	Ser	Met	Met	Met	Leu	Gly	Glu	Ala	Glu	Glu	Ile	
80			185				190				195						
82	aga	gac	atc	gct	cgc	gag	gtt	ctt	aag	atc	ttt	ggc	gaa	tac	agc	ctc	677
83	Arg	Asp	Ile	Ala	Arg	Glu	Val	Leu	Lys	Ile	Phe	Gly	Glu	Tyr	Ser	Leu	
84		200				205				210							
86	act	gac	ttc	atc	tgg	cca	ttg	aag	cat	ctc	aag	gtt	gga	aag	tat	gag	725
87	Thr	Asp	Phe	Ile	Trp	Pro	Leu	Lys	His	Leu	Lys	Val	Gly	Lys	Tyr	Glu	
88	215				220					225					230		
90	aag	agg	atc	gac	gac	atc	ttg	aac	aag	ttc	gac	cct	gtc	gtt	gaa	agg	773
91	Lys	Arg	Ile	Asp	Asp	Ile	Leu	Asn	Lys	Phe	Asp	Pro	Val	Val	Glu	Arg	
92				235				240						245			
94	gtc	atc	aag	aag	cgc	cgt	gag	atc	gtg	agg	agg	aga	aag	aac	gga	gag	821
95	Val	Ile	Lys	Lys	Arg	Arg	Glu	Ile	Val	Arg	Arg	Arg	Lys	Asn	Gly	Glu	
96			250				255						260				
98	gtt	gtt	gag	ggt	gag	gtc	agc	ggg	gtt	ttc	ctt	gac	act	ttg	ctt	gaa	869
99	Val	Val	Glu	Gly	Glu	Val	Ser	Gly	Val	Phe	Leu	Asp	Thr	Leu	Leu	Glu	
100			265			270				275							
102	ttc	gct	gag	gat	gag	acc	atg	gag	atc	aaa	atc	acc	aag	gac	cac	atc	917
103	Phe	Ala	Glu	Asp	Glu	Thr	Met	Glu	Ile	Lys	Ile	Thr	Lys	Asp	His	Ile	
104		280				285				290							
106	aag	ggt	ctt	gtt	gtc	gac	ttt	ttc	tcg	gca	gga	aca	gac	tcc	aca	gcg	965
107	Lys	Gly	Leu	Val	Val	Asp	Phe	Phe	Ser	Ala	Gly	Thr	Asp	Ser	Thr	Ala	
108	295				300					305					310		
110	gtg	gca	aca	gag	tgg	gca	ttg	gca	gaa	ctc	atc	aac	aat	cct	aag	gtg	1013
111	Val	Ala	Thr	Glu	Trp	Ala	Leu	Ala	Glu	Leu	Ile	Asn	Asn	Pro	Lys	Val	
112				315						320					325		
114	ttg	gaa	aag	gct	cgt	gag	gag	gtc	tac	agt	gtt	gtg	gga	aag	gac	aga	1061
115	Leu	Glu	Lys	Ala	Arg	Glu	Glu	Val	Tyr	Ser	Val	Val	Gly	Lys	Asp	Arg	
116			330					335					340				
118	ctt	gtg	gac	gaa	gtt	gac	act	caa	aac	ctt	cct	tac	att	aga	gca	atc	1109
119	Leu	Val	Asp	Glu	Val	Asp	Thr	Gln	Asn	Leu	Pro	Tyr	Ile	Arg	Ala	Ile	
120			345				350						355				
122	gtg	aag	gag	aca	ttc	cgc	atg	cac	ccg	cca	ctc	cca	gtg	gtc	aaa	aga	1157
123	Val	Lys	Glu	Thr	Phe	Arg	Met	His	Pro	Pro	Leu	Pro	Val	Val	Lys	Arg	
124		360				365				370							
126	aag	tgc	aca	gaa	gag	tgt	gag	att	aat	gga	tat	gtg	atc	cca	gag	gga	1205
127	Lys	Cys	Thr	Glu	Glu	Cys	Glu	Ile	Asn	Gly	Tyr	Val	Ile	Pro	Glu	Gly	
128	375				380					385					390		
130	gca	ttg	att	ctc	ttc	aat	gta	tgg	caa	gta	gga	aga	gac	ccc	aaa	tac	1253
131	Ala	Leu	Ile	Leu	Phe	Asn	Val	Trp	Gln	Val	Gly	Arg	Asp	Pro	Lys	Tyr	
132				395				400						405			

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134 tgg gac aga cca tcg gag ttc cgt cct gag agg ttc cta gag aca ggg 1301
135 Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu Arg Phe Leu Glu Thr Gly
136          410          415          420
138 gct gaa ggg gaa gca ggg cct ctt gat ctt agg gga caa cat ttt caa 1349
139 Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu Arg Gly Gln His Phe Gln
140          425          430          435
142 ctt ctc cca ttt ggg tct ggg agg aga atg tgc cct gga gtc aat ctg 1397
143 Leu Leu Pro Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Val Asn Leu
144          440          445          450
146 gct act tcg gga atg gca aca ctt ctt gca tct ctt att cag tgc ttc 1445
147 Ala Thr Ser Gly Met Ala Thr Leu Leu Ala Ser Leu Ile Gln Cys Phe
148 455          460          465          470
150 gac ttg caa gtg ctg ggt cca caa gga cag ata ttg aag ggt ggt gac 1493
151 Asp Leu Gln Val Leu Gly Pro Gln Gly Gln Ile Leu Lys Gly Gly Asp
152          475          480          485
154 gcc aaa gtt agc atg gaa gag aga gcc ggc ctc act gtt cca agg gca 1541
155 Ala Lys Val Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala
156          490          495          500
158 cat agt ctt gtc tgt gtt cca ctt gca agg atc ggc gtt gca tct aaa 1589
159 His Ser Leu Val Cys Val Pro Leu Ala Arg Ile Gly Val Ala Ser Lys
160          505          510          515
162 ctc ctt tct taattaagat catcgatcatc atcatcatat gtaatattta 1638
163 Leu Leu Ser
164          520
166 ctttttgtgt gttgataatc atcatttcaa taagggtctca ttcattctact ttttatgaag 1698
168 tatataagcc cttccatgc 1717
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172 <211> LENGTH: 521
173 <212> TYPE: PRT
174 <213> ORGANISM: Glycine max
176 <400> SEQUENCE: 2
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181          20          25          30
183 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
184          35          40          45
186 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
187          50          55          60
189 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
190 65          70          75          80
192 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
193          85          90          95
195 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
196          100          105          110
198 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
199          115          120          125
201 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
202          130          135          140

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204 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
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207 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
208 165 170 175
210 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
211 180 185 190
213 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
214 195 200 205
216 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
217 210 215 220
219 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
220 225 230 235 240
222 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
223 245 250 255
225 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
226 260 265 270
228 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
229 275 280 285
231 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
232 290 295 300
234 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
235 305 310 315 320
237 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
238 325 330 335
240 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
241 340 345 350
243 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
244 355 360 365
246 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
247 370 375 380
249 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
250 385 390 395 400
252 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
253 405 410 415
255 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
256 420 425 430
258 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
259 435 440 445
261 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
262 450 455 460
264 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
265 465 470 475 480
267 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
268 485 490 495
270 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
271 500 505 510
273 Ile Gly Val Ala Ser Lys Leu Leu Ser
274 515 520
278 <210> SEQ ID NO: 3

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279 <211> LENGTH: 523
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288      20          25          30
290 Pro Pro Ser Pro Phe Phe Arg Leu Pro Ile Ile Gly His Met His Met
291      35          40          45
293 Leu Gly Pro Leu Leu His Gln Ser Phe His Asn Leu Ser His Arg Tyr
294      50          55          60
296 Gly Pro Leu Phe Ser Leu Asn Phe Gly Ser Val Leu Cys Val Val Ala
297      65          70          75          80
299 Ser Thr Pro His Phe Ala Lys Gln Leu Leu Gln Thr Asn Glu Leu Ala
300      85          90          95
302 Phe Asn Cys Arg Ile Glu Ser Thr Ala Val Lys Lys Leu Thr Tyr Glu
303      100         105         110
305 Ser Ser Leu Ala Phe Ala Pro Tyr Gly Asp Tyr Trp Arg Phe Ile Lys
306      115         120         125
308 Lys Leu Ser Met Asn Glu Leu Leu Gly Ser Arg Ser Ile Asn Asn Phe
309      130         135         140
311 Gln His Leu Arg Ala Gln Glu Thr His Gln Leu Leu Arg Leu Leu Ser
312      145         150         155         160
314 Asn Arg Ala Arg Ala Phe Glu Ala Val Asn Ile Thr Glu Glu Leu Leu
315      165         170         175
317 Lys Leu Thr Asn Asn Val Ile Ser Ile Met Met Val Gly Glu Ala Glu
318      180         185         190
320 Glu Ala Arg Asp Val Val Arg Asp Val Thr Glu Ile Phe Gly Glu Phe
321      195         200         205
323 Asn Val Ser Asp Phe Ile Trp Leu Phe Lys Lys Met Asp Leu Gln Gly
324      210         215         220
326 Phe Gly Lys Arg Ile Glu Asp Leu Phe Gln Arg Phe Asp Thr Leu Val
327      225         230         235         240
329 Glu Arg Ile Ile Ser Lys Arg Glu Gln Thr Arg Lys Asp Arg Arg Arg
330      245         250         255
332 Asn Gly Lys Lys Gly Glu Gln Gly Ser Gly Asp Gly Ile Arg Asp Phe
333      260         265         270
335 Leu Asp Ile Leu Leu Asp Cys Thr Glu Asp Glu Asn Ser Glu Ile Lys
336      275         280         285
338 Ile Gln Arg Val His Ile Lys Ala Leu Ile Met Asp Phe Phe Thr Ala
339      290         295         300
341 Gly Thr Asp Thr Thr Ala Ile Ser Thr Glu Trp Ala Leu Val Glu Leu
342      305         310         315         320
344 Val Lys Lys Pro Ser Val Leu Gln Lys Val Arg Glu Glu Ile Asp Asn
345      325         330         335
347 Val Val Gly Lys Asp Arg Leu Val Glu Glu Ser Asp Cys Pro Asn Leu
348      340         345         350
350 Pro Tyr Leu Gln Ala Ile Leu Lys Glu Thr Phe Arg Leu His Pro Pro

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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date